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## **Supplemental Material**

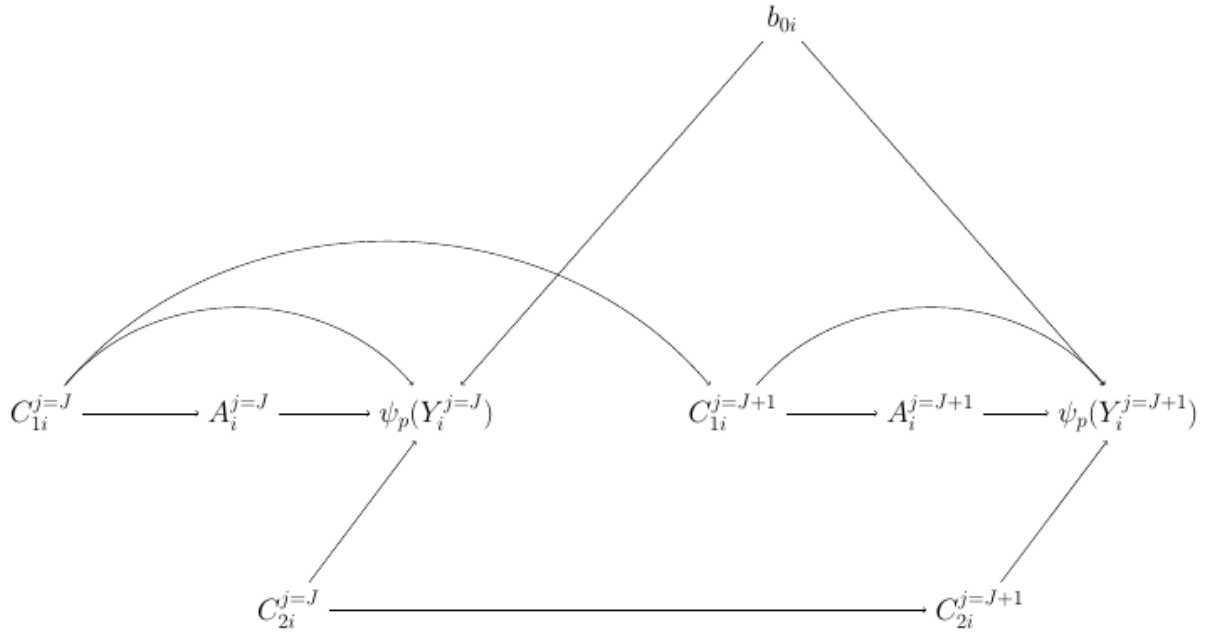
### **Beyond the Mean: Quantile Regression to Explore the Association of Air Pollution with Gene-Specific Methylation in the Normative Aging Study**

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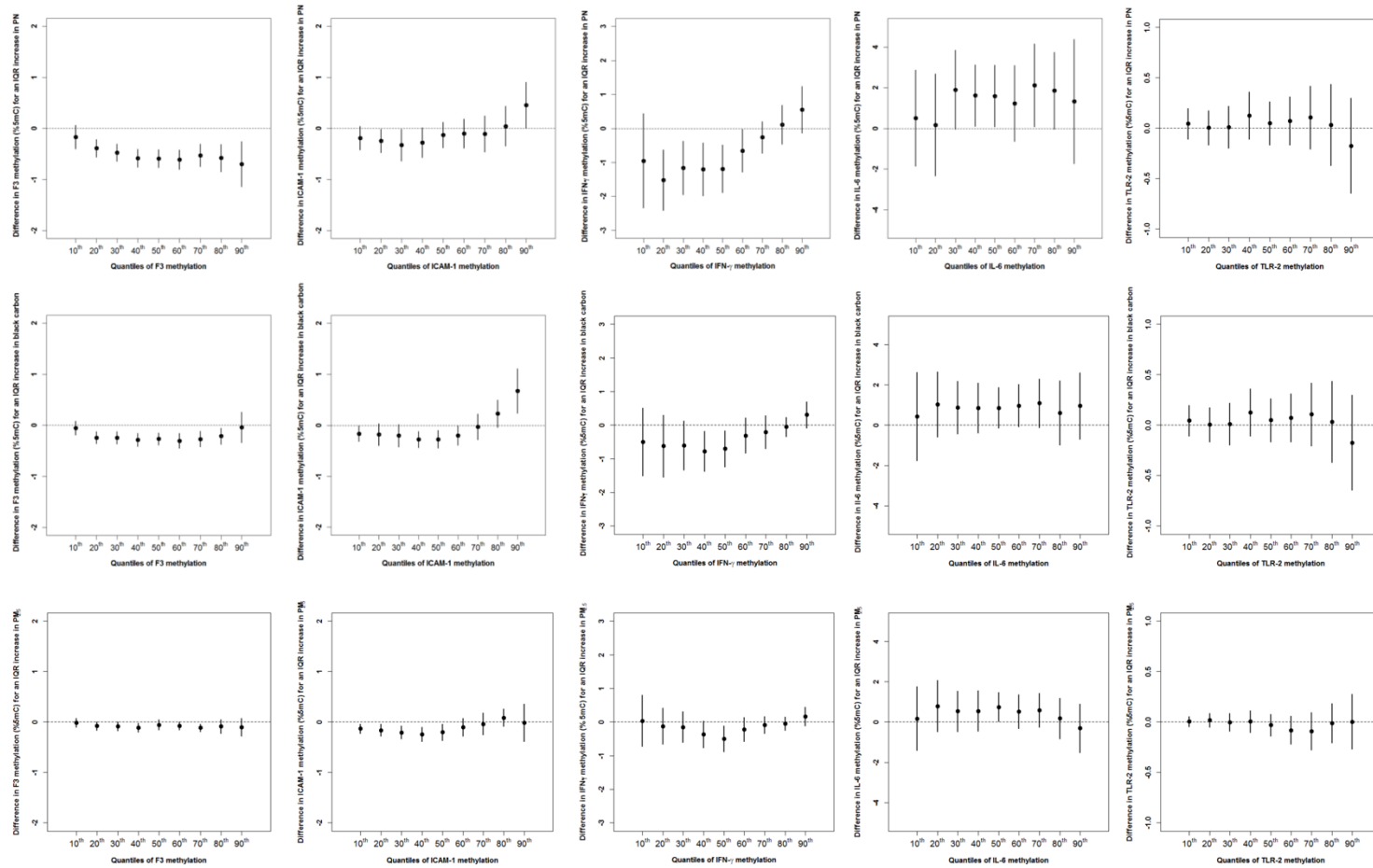
#### **Table of Contents**

**Figure S1.** Directed Acyclic Graph (DAG) at adjacent visits  $j=J$  and  $j=J+1$ . This DAG illustrates the relationships we assumed between the variables included in the regression models.  $A_i^j$  represents the 4-week moving average of air pollutant concentration before the  $j^{\text{th}}$  visit of participant  $i$ .  $Y_i^j$  represents the  $i^{\text{th}}$  participant gene-specific DNA methylation at visit  $j$ .  $\psi_p(Y_i^j)$  is the  $p^{\text{th}}$  quantile of the  $Y_{ij}$  distribution.  $C_{1i}^j$  and  $C_{2i}^j$  correspond to the potential confounding variables and risk factors of DNA methylation for participant  $i^{\text{th}}$  at visit  $j$ , respectively.  $b_{0i}$  represents the random intercept of participant  $i$ .

**Figure S2.** Sensitivity analyses restricted to never and former smokers: absolute difference in gene-specific methylation (expressed in %5mC with 95%CI) associated with an IQR increase in exposure (IQR=14,599 number per  $\text{cm}^3$  for particle number,  $0.26 \mu\text{g}/\text{m}^3$  for  $\text{PM}_{2.5}$  black carbon, and  $3.4 \mu\text{g}/\text{m}^3$  for  $\text{PM}_{2.5}$  mass), according to deciles of the methylation distribution. In this secondary analysis, we considered only never and former smokers based on the time-varying smoking status variable. The analysis included 755 participants and 1,737 individual observations.



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